

RAW SEQUENCE LISTING
PATENT APPLICATION US/07/923,692CDATE: 10/28/93
TIME: 14:00:53

INPUT SET: S6832.raw

SEQUENCE LISTING

(1) General Information:

(i) APPLICANT: Donson, Jon
Dawson, William O.
Grantham, George L.
Turpen, Thomas H.
Turpen, Ann Myers
Garger, Stephen J.
Grill, Laurence K.

(ii) TITLE OF INVENTION: RECOMBINANT PLANT VIRAL NUCLEIC ACIDS

(iii) NUMBER OF SEQUENCES: 11

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Limbach & Limbach
(B) STREET: 2001 Ferry Building
(C) CITY: San Francisco
(D) STATE: CAL
(F) ZIP: 94111

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: Patent in Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 923,692
(B) FILING DATE: 31-JUL-1992
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 600,244
(B) FILING DATE: 22-OCT-1990

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 641,617
(B) FILING DATE: 16-JAN-1991

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 310,881
(B) FILING DATE: 17-FEB-1989

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 160,766
(B) FILING DATE: 26-FEB-1988

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 160,771

see p. 12

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52 (B) FILING DATE: 26-FEB-1988
53
54 (vii) PRIOR APPLICATION DATA:
55 (A) APPLICATION NUMBER: US 347,637
56 (B) FILING DATE: 05-MAY-1989
57
58 (vii) PRIOR APPLICATION DATA:
59 (A) APPLICATION NUMBER: US 363,138
60 (B) FILING DATE: 08-JUN-1989
61
62 (vii) PRIOR APPLICATION DATA:
63 (A) APPLICATION NUMBER: US 219,279
64 (B) FILING DATE: 15-JUL-1988
65
66 (viii) ATTORNEY/AGENT INFORMATION:
67 (A) NAME: Halluin, Albert P.
68 (B) REGISTRATION NUMBER: 28,957
69 (C) REFERENCE/DOCKET NUMBER: BIOG-20121
70 USA
71
72 (ix) TELECOMMUNICATION INFORMATION:
73 (A) TELEPHONE: 415-433-4150
74 (B) TELEFAX: 415-433-8716
75
76
77 (2) INFORMATION FOR SEQ ID NO: 1:
78
79 (i) SEQUENCE CHARACTERISTICS:
80 (A) LENGTH: 4 amino acids
81 (B) TYPE: amino acid
82 (D) TOPOLOGY: linear
83
84 (ii) MOLECULE TYPE: peptide
85
86 (iii) HYPOTHETICAL: NO
87
88 (iv) ANTI-SENSE: NO
89
90 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
91
92 Pro Xaa Gly Pro
93 1
94
95 (2) INFORMATION FOR SEQ ID NO: 2:
96
97 (i) SEQUENCE CHARACTERISTICS:
98 (A) LENGTH: 13 base pairs
99 (B) TYPE: nucleic acid
100 (C) STRANDEDNESS: single
101 (D) TOPOLOGY: linear
102

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103 (ii) MOLECULE TYPE: DNA (genomic)
104
105 (iii) HYPOTHETICAL: NO
106
107 (iv) ANTI-SENSE: NO
108
109 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
110
111 GGGTACCTGG GCC 13
112
113
114
115 (2) INFORMATION FOR SEQ ID NO: 3:
116
117 (i) SEQUENCE CHARACTERISTICS:
118 (A) LENGTH: 886 base pairs
119 (B) TYPE: nucleic acid
120 (C) STRANDEDNESS: single
121 (D) TOPOLOGY: linear
122
123 (ii) MOLECULE TYPE: DNA (genomic)
124
125 (iii) HYPOTHETICAL: NO
126
127 (iv) ANTI-SENSE: NO
128
129 (vi) ORIGINAL SOURCE:
130 (A) ORGANISM: Chinese cucumber
131
132 (vii) IMMEDIATE SOURCE:
133 (B) CLONE: alpha-trichosanthin
134
135 (ix) FEATURE:
136 (A) NAME/KEY: CDS (B) LOCATION: 8. .877
137 (B) LOCATION: 8. .877
138
139 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
140
141 CTCGAGG ATG ATC AGA TTC TTA GTC CTC TCT TTG CTA ATT CTC ACC CTC 49
142
143 Met Ile Arg Phe Leu Val Leu Ser Leu Leu Ile Leu Thr Leu
144 1 5 10
145
146 TTC CTA ACA ACT CCT GCT GTG GAG GGC GAT GTT AGC TTC CGT TTA TCA 97
147
148 Phe Leu Thr Thr Pro Ala Val Glu Gly Asp Val Ser Phe Arg Leu Ser
149 15 20 25 30
150
151 GGT GCA ACA AGC AGT TCC TAT GGA GTT TTC ATT TCA AAT CTG AGA AAA 145
152
153 Gly Ala Thr Ser Ser Ser Tyr Gly Val Phe Ile Ser Asn Leu Arg Lys

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| | | | | | | | | |
|-----|---|-----|--|-----|--|-----|--|-----|
| 154 | | 35 | | 40 | | 45 | | |
| 155 | | | | | | | | |
| 156 | GCT CTT CCA AAT GAA AGG AAA CTG TAC GAT ATC CCT CTG TTA CGT TCC | | | | | | | 193 |
| 157 | | | | | | | | |
| 158 | Ala Leu Pro Asn Glu Arg Lys Leu Tyr Asp Ile Pro Leu Leu Arg Ser | | | | | | | |
| 159 | | 50 | | 55 | | 60 | | |
| 160 | | | | | | | | |
| 161 | TCT CTT CCA GGT TCT CAA CGC TAC GCA TTG ATC CAT CTC ACA AAT TAC | | | | | | | 241 |
| 162 | | | | | | | | |
| 163 | Ser Leu Pro Gly Ser Gln Arg Tyr Ala Leu Ile His Leu Thr Asn Tyr | | | | | | | |
| 164 | | 65 | | 70 | | 75 | | |
| 165 | | | | | | | | |
| 166 | GCC GAT GAA ACC ATT TCA GTG GCC ATA GAC GTA ACG AAC GTC TAT ATT | | | | | | | 289 |
| 167 | | | | | | | | |
| 168 | Ala Asp Glu Thr Ile Ser Val Ala Ile Asp Val Thr Asn Val Tyr Ile | | | | | | | |
| 169 | | 80 | | 85 | | 90 | | |
| 170 | | | | | | | | |
| 171 | ATG GGA TAT CGC GCT GGC GAT ACA TCC TAT TTT TTC AAC GAG GCT TCT | | | | | | | 337 |
| 172 | | | | | | | | |
| 173 | Met Gly Tyr Arg Ala Gly Asp Thr Ser Tyr Phe Phe Asn Glu Ala Ser | | | | | | | |
| 174 | | 95 | | 100 | | 105 | | 110 |
| 175 | | | | | | | | |
| 176 | GCA ACA GAA GCT GCA AAA TAT GTA TTC AAA GAC GCT ATG CGA AAA GTT | | | | | | | 385 |
| 177 | | | | | | | | |
| 178 | Ala Thr Glu Ala Ala Lys Tyr Val Phe Lys Asp Ala Met Arg Lys Val | | | | | | | |
| 179 | | 115 | | 120 | | 125 | | |
| 180 | | | | | | | | |
| 181 | ACG CTT CCA TAT TCT GGC AAT TAC GAA AGG CTT CAA ACT GCT GCG GGC | | | | | | | 433 |
| 182 | | | | | | | | |
| 183 | Thr Leu Pro Tyr Ser Gly Asn Tyr Glu Arg Leu Gln Thr Ala Ala Gly | | | | | | | |
| 184 | | 130 | | 135 | | 140 | | |
| 185 | | | | | | | | |
| 186 | AAA ATA AGG GAA AAT ATT CCG CTT GGA CTC CCA GCT TTG GAC AGT GCC | | | | | | | 481 |
| 187 | | | | | | | | |
| 188 | Lys Ile Arg Glu Asn Ile Pro Leu Gly Leu Pro Ala Leu Asp Ser Ala | | | | | | | |
| 189 | | 145 | | 150 | | 155 | | |
| 190 | | | | | | | | |
| 191 | ATT ACC ACT TTG TTT TAC TAC AAC GCC AAT TCT GCT GCG TCG GCA CTT | | | | | | | 529 |
| 192 | | | | | | | | |
| 193 | Ile Thr Thr Leu Phe Tyr Tyr Asn Ala Asn Ser Ala Ala Ser Ala Leu | | | | | | | |
| 194 | | 160 | | 165 | | 170 | | |
| 195 | | | | | | | | |
| 196 | ATG GTA CTC ATT CAG TCG ACG TCT GAG GCT GCG AGG TAT AAA TTT ATT | | | | | | | 577 |
| 197 | | | | | | | | |
| 198 | Met Val Leu Ile Gln Ser Thr Ser Glu Ala Ala Arg Tyr Lys Phe Ile | | | | | | | |
| 199 | | 175 | | 180 | | 185 | | 190 |
| 200 | | | | | | | | |
| 201 | GAG CAA CAA ATT GGG AAG CGC GTT GAC AAA ACC TTC CTA CCA AGT TTA | | | | | | | 625 |
| 202 | | | | | | | | |
| 203 | Glu Gln Gln Ile Gly Lys Arg Val Asp Lys Thr Phe Leu Pro Ser Leu | | | | | | | |
| 204 | | 195 | | 200 | | 205 | | |

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205
206 GCA ATT ATA AGT TTG GAA AAT AGT TGG TCT GCT CTC TCC AAG CAA ATT 673
207
208 Ala Ile Ile Ser Leu Glu Asn Ser Trp Ser Ala Leu Ser Lys Gln Ile
209 210 215 220
210
211 CAG ATA GCG AGT ACT AAT AAT GGA CAG TTT GAA ACT CCT GTT GTG CTT 721
212
213 Gln Ile Ala Ser Thr Asn Asn Gly Gln Phe Glu Thr Pro Val Val Leu
214 225 230 235
215
216 ATA AAT GCT CAA AAC CAA CGA GTC ATG ATA ACC AAT GTT GAT GCT GGA 769
217
218 Ile Asn Ala Gln Asn Gln Arg Val Met Ile Thr Asn Val Asp Ala Gly
219 240 245 250
220
221 GTT GTA ACC TCC AAC ATC GCG TTG CTG CTG AAT CGA AAC AAT ATG GCA 817
222
223 Val Val Thr Ser Asn Ile Ala Leu Leu Leu Asn Arg Asn Asn Met Ala
224 255 260 265 270
225
226 GCC ATG GAT GAC GAT GTT CCT ATG ACA CAG AGC TTT GGA TGT GGA AGT 865
227
228 Ala Met Asp Asp Asp Val Pro Met Thr Gln Ser Phe Gly Cys Gly Ser
229 275 280 285
230
231 TAT GCT ATT TAGTAACTCG AG 886
232
233 Tyr Ala Ile
234 290
235
236
237 (2) INFORMATION FOR SEQ ID NO:4:
238
239 (i) SEQUENCE CHARACTERISTICS:
240 (A) LENGTH: 289 amino acids
241 (B) TYPE: amino acid
242 (D) TOPOLOGY: linear
243
244 (ii) MOLECULE TYPE: protein
245
246 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
247
248
249 Met Ile Arg Phe Leu Val Leu Ser Leu Leu Ile Leu Thr Leu Phe Leu
250 1 5 10 15
251
252 Thr Thr Pro Ala Val Glu Gly Asp Val Ser Phe Arg Leu Ser Gly Ala
253 20 25 30
254
255 Thr Ser Ser Ser Tyr Gly Val Phe Ile Ser Asn Leu Arg Lys Ala Leu

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| | | | |
|-----|---|-----|---------|
| 256 | 35 | 40 | 45 |
| 257 | | | |
| 258 | Pro Asn Glu Arg Lys Leu Tyr Asp Ile Pro Leu Leu Arg Ser Ser Leu | | |
| 259 | 50 | 55 | 60 |
| 260 | | | |
| 261 | Pro Gly Ser Gln Arg Tyr Ala Leu Ile His Leu Thr Asn Tyr Ala Asp | | |
| 262 | 65 | 70 | 75 80 |
| 263 | | | |
| 264 | Glu Thr Ile Ser Val Ala Ile Asp Val Thr Asn Val Tyr Ile Met Gly | | |
| 265 | 85 | 90 | 95 |
| 266 | | | |
| 267 | Tyr Arg Ala Gly Asp Thr Ser Tyr Phe Phe Asn Glu Ala Ser Ala Thr | | |
| 268 | 100 | 105 | 110 |
| 269 | | | |
| 270 | Glu Ala Ala Lys Tyr Val Phe Lys Asp Ala Met Arg Lys Val Thr Leu | | |
| 271 | 115 | 120 | 125 |
| 272 | | | |
| 273 | Pro Tyr Ser Gly Asn Tyr Glu Arg Leu Gln Thr Ala Ala Gly Lys Ile | | |
| 274 | 130 | 135 | 140 |
| 275 | | | |
| 276 | Arg Glu Asn Ile Pro Leu Gly Leu Pro Ala Leu Asp Ser Ala Ile Thr | | |
| 277 | 145 | 150 | 155 160 |
| 278 | | | |
| 279 | Thr Leu Phe Tyr Tyr Asn Ala Asn Ser Ala Ala Ser Ala Leu Met Val | | |
| 280 | 165 | 170 | 175 |
| 281 | | | |
| 282 | Leu Ile Gln Ser Thr Ser Glu Ala Ala Arg Tyr Lys Phe Ile Glu Gln | | |
| 283 | 180 | 185 | 190 |
| 284 | | | |
| 285 | Gln Ile Gly Lys Arg Val Asp Lys Thr Phe Leu Pro Ser Leu Ala Ile | | |
| 286 | 195 | 200 | 205 |
| 287 | | | |
| 288 | Ile Ser Leu Glu Asn Ser Trp Ser Ala Leu Ser Lys Gln Ile Gln Ile | | |
| 289 | 210 | 215 | 220 |
| 290 | | | |
| 291 | Ala Ser Thr Asn Asn Gly Gln Phe Glu Thr Pro Val Val Leu Ile Asn | | |
| 292 | 225 | 230 | 235 240 |
| 293 | | | |
| 294 | Ala Gln Asn Gln Arg Val Met Ile Thr Asn Val Asp Ala Gly Val Val | | |
| 295 | 245 | 250 | 255 |
| 296 | | | |
| 297 | Thr Ser Asn Ile Ala Leu Leu Leu Asn Arg Asn Asn Met Ala Ala Met | | |
| 298 | 260 | 265 | 270 |
| 299 | | | |
| 300 | Asp Asp Asp Val Pro Met Thr Gln Ser Phe Gly Cys Gly Ser Tyr Ala | | |
| 301 | 275 | 280 | 285 |
| 302 | Ile | | |
| 303 | | | |
| 304 | | | |
| 305 | (2) INFORMATION FOR SEQ ID NO: 5: | | |
| 306 | | | |

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307      (i)      SEQUENCE CHARACTERISTICS:
308              (A) LENGTH: 1450 base pairs
309              (B) TYPE: nucleic acid
310              (C) STRANDEDNESS: single
311              (D) TOPOLOGY: linear
312
313      (ii)      MOLECULE TYPE: DNA (genomic)
314
315      (iii)     HYPOTHETICAL: NO
316
317      (iv)      ANTI-SENSE: NO
318
319      (vi)      ORIGINAL SOURCE:
320              (A) ORGANISM: Oryza sativa
321
322      (vii)     IMMEDIATE SOURCE:
323              (B) CLONE: alpha-amylase
324
325      (ix)      FEATURE:
326              (A) NAME/KEY: CDS (B) LOCATION: 12. .1316
327              (B) LOCATION: 12. .1316
328
329      (xi)      SEQUENCE DESCRIPTION: SEQ ID NO: 5:
330
331      CCTCGAGGTG C ATG CAG GTG CTG AAC ACC ATG GTG AAC A CAC TTC TTG      48
332
333              Met Gln Val Leu Asn Thr Met Val Asn Lys His Phe Leu
334              1              5              10
335
336      TCC CTT TCG GTC CTC ATC GTC CTC CTT GGC CTC TCC TCC AAC TTG ACA      96
337
338      Ser Leu Ser Val Leu Ile Val Leu Leu Gly Leu Ser Ser Asn Leu Thr
339              15              20              25
340
341      GCC GGG CAA GTC CTG TTT CAG GGA TTC AAC TGG GAG TCG TGG AAG GAG      144
342
343      Ala Gly Gln Val Leu Phe Gln Gly Phe Asn Trp Glu Ser Trp Lys Glu
344              30              35              40              45
345
346      AAT GGC GGG TGG TAC AAC TTC CTG ATG GGC AAG GTG GAC GAC ATC GCC      192
347
348      Asn Gly Gly Trp Tyr Asn Phe Leu Met Gly Lys Val Asp Asp Ile Ala
349              50              55              60
350
351      GCA GCC GGC ATC ACC CAC GTC TGG CTC CCT CCG CCG TCT CAC TCT GTC      240
352
353      Ala Ala Gly Ile Thr His Val Trp Leu Pro Pro Pro Ser His Ser Val
354              65              70              75
355
356      GGC GAG CAA GGC TAC ATG CCT GGG CGG CTG TAC GAT CTG GAC GCG TCT      288
357

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| | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 358 | Gly | Glu | Gln | Gly | Tyr | Met | Pro | Gly | Arg | Leu | Tyr | Asp | Leu | Asp | Ala | Ser | |
| 359 | | | 80 | | | | | 85 | | | | | 90 | | | | |
| 360 | | | | | | | | | | | | | | | | | |
| 361 | AAG | TAC | GGC | AAC | GAG | GCG | CAG | CTC | AAG | TCG | CTG | ATC | GAG | GCG | TTC | CAT | 336 |
| 362 | | | | | | | | | | | | | | | | | |
| 363 | Lys | Tyr | Gly | Asn | Glu | Ala | Gln | Leu | Lys | Ser | Leu | Ile | Glu | Ala | Phe | His | |
| 364 | | 95 | | | | | 100 | | | | | 105 | | | | | |
| 365 | | | | | | | | | | | | | | | | | |
| 366 | GGC | AAG | GGC | GTC | CAG | GTG | ATC | GCC | GAC | ATC | GTC | ATC | AAC | CAC | CGC | ACG | 384 |
| 367 | | | | | | | | | | | | | | | | | |
| 368 | Gly | Lys | Gly | Val | Gln | Val | Ile | Ala | Asp | Ile | Val | Ile | Asn | His | Arg | Thr | |
| 369 | 110 | | | | | 115 | | | | | 120 | | | | | 125 | |
| 370 | | | | | | | | | | | | | | | | | |
| 371 | GCG | GAG | CAC | AAG | GAC | GGC | CGC | GGC | ATC | TAC | TGC | CTC | TTC | GAG | GGC | GGG | 432 |
| 372 | | | | | | | | | | | | | | | | | |
| 373 | Ala | Glu | His | Lys | Asp | Gly | Arg | Gly | Ile | Tyr | Cys | Leu | Phe | Glu | Gly | Gly | |
| 374 | | | | | 130 | | | | | 135 | | | | | 140 | | |
| 375 | | | | | | | | | | | | | | | | | |
| 376 | ACG | CCC | GAC | TCC | CGC | CTC | GAC | TGG | GGC | CCG | CAC | ATG | ATC | TGC | CGC | GAC | 480 |
| 377 | | | | | | | | | | | | | | | | | |
| 378 | Thr | Pro | Asp | Ser | Arg | Leu | Asp | Trp | Gly | Pro | His | Met | Ile | Cys | Arg | Asp | |
| 379 | | | | 145 | | | | | 150 | | | | | 155 | | | |
| 380 | | | | | | | | | | | | | | | | | |
| 381 | GAC | CCC | TAC | GGC | CAT | GGC | ACC | GGC | AAC | CCG | GAC | ACC | GGC | GCC | GAC | TTC | 528 |
| 382 | | | | | | | | | | | | | | | | | |
| 383 | Asp | Pro | Tyr | Gly | Asp | Gly | Thr | Gly | Asn | Pro | Asp | Thr | Gly | Ala | Asp | Phe | |
| 384 | | | 160 | | | | | 165 | | | | | 170 | | | | |
| 385 | | | | | | | | | | | | | | | | | |
| 386 | GCC | GCC | GCG | CCG | GAC | ATC | GAC | CAC | CTC | AAC | AAG | CGC | GTC | CAG | CGG | GAG | 576 |
| 387 | | | | | | | | | | | | | | | | | |
| 388 | Ala | Ala | Ala | Pro | Asp | Ile | Asp | His | Leu | Asn | Lys | Arg | Val | Gln | Arg | Glu | |
| 389 | | 175 | | | | | 180 | | | | | 185 | | | | | |
| 390 | | | | | | | | | | | | | | | | | |
| 391 | CTC | ATT | GGC | TGG | CTC | GAC | TGG | CTC | AAG | ATG | GAC | ATC | GGC | TTC | GAC | GCG | 624 |
| 392 | | | | | | | | | | | | | | | | | |
| 393 | Leu | Ile | Gly | Trp | Leu | Asp | Trp | Leu | Lys | Met | Asp | Ile | Gly | Phe | Asp | Ala | |
| 394 | 190 | | | | | 195 | | | | | 200 | | | | | 205 | |
| 395 | | | | | | | | | | | | | | | | | |
| 396 | TGG | CGC | CTC | GAC | TTC | GCC | AAG | GGC | TAC | TCC | GCC | GAC | ATG | GCA | AAC | ATC | 672 |
| 397 | | | | | | | | | | | | | | | | | |
| 398 | Trp | Arg | Leu | Asp | Phe | Ala | Lys | Gly | Tyr | Ser | Ala | Asp | Met | Ala | Lys | Ile | |
| 399 | | | | 210 | | | | | | 215 | | | | | 220 | | |
| 400 | | | | | | | | | | | | | | | | | |
| 401 | TAC | ATC | GAC | GCC | ACC | GAG | CCG | AGC | TTC | GCC | GTG | CCC | GAG | ATA | TCG | ACG | 720 |
| 402 | | | | | | | | | | | | | | | | | |
| 403 | Tyr | Ile | Asp | Ala | Thr | Glu | Pro | Ser | Phe | Ala | Val | Ala | Glu | Ile | Trp | Thr | |
| 404 | | | | 225 | | | | | 230 | | | | | 235 | | | |
| 405 | | | | | | | | | | | | | | | | | |
| 406 | TCC | ATG | GCG | AAC | GGC | GGG | GAC | GGC | AAG | CCG | AAC | TAC | GAC | CAG | AAC | GCG | 768 |
| 407 | | | | | | | | | | | | | | | | | |
| 408 | Ser | Met | Ala | Asn | Gly | Gly | Asp | Gly | Lys | Pro | Asn | Tyr | Asp | Gln | Asn | Ala | |

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|-----|---|------|-----|--|
| 409 | 240 | 245 | 250 | |
| 410 | | | | |
| 411 | CAC CGG CAG GAG CTG GTC AAC TGG GTC GAT CGT GTC GGC GGC GCC AAC | 816 | | |
| 412 | | | | |
| 413 | His Arg Gln Glu Leu Val Asn Trp Val Asp Arg Val Gly Gly Ala Asn | | | |
| 414 | 255 260 265 | | | |
| 415 | | | | |
| 416 | ACC AAC GGC ACG GCG TTC GAC TTC ACC ACC AAG GGC ATC CTC AAC GTC | 864 | | |
| 417 | | | | |
| 418 | Ser Asn Gly Thr Ala Phe Asp Phe Thr Thr Lys Gly Ile Leu Asn Val | | | |
| 419 | 270 275 280 285 | | | |
| 420 | | | | |
| 421 | GCC GTG GAG GGC GAG CTG TGG CGC CTC CGC GGC GAG GAC GGC AAG GCG | 912 | | |
| 422 | | | | |
| 423 | Ala Val Glu Gly Glu Leu Trp Arg Leu Arg Gly Glu Asp Gly Lys Ala | | | |
| 424 | 290 295 300 | | | |
| 425 | | | | |
| 426 | CCC GGC ATG ATC GGG TGC TGG CCG GCC AAG GCG ACG ACC TTC GTC GAC | 960 | | |
| 427 | | | | |
| 428 | Pro Gly Met Ile Gly Trp Trp Pro Ala Lys Ala Thr Thr Phe Val Asp | | | |
| 429 | 305 310 315 | | | |
| 430 | | | | |
| 431 | AAC CAC GAC ACC GGC TCG ACG CAG CAC CTG TGG CCG TTC CCC TCC GAC | 1008 | | |
| 432 | | | | |
| 433 | Asn His Asp Thr Gly Ser Thr Gln His Leu Trp Pro Phe Pro Ser Asp | | | |
| 434 | 320 325 330 | | | |
| 435 | | | | |
| 436 | AAG GTC ATG CAG GGC TAC GCA TAC ATC CTC ACC CAC CCC GGC AAC CCA | 1056 | | |
| 437 | | | | |
| 438 | Lys Val Met Gln Gly Tyr Ala Tyr Ile Leu Thr His Pro Gly Asn Pro | | | |
| 439 | 335 340 345 | | | |
| 440 | | | | |
| 441 | TGC ATC TTG TAC GAC CAT TTC TTC GAT TGG GGT CTC AAG GAG GAG ATC | 1104 | | |
| 442 | | | | |
| 443 | Cys Ile Phe Tyr Asp His Phe Phe Asp Trp Gly Leu Lys Glu Glu Ile | | | |
| 444 | 350 355 360 365 | | | |
| 445 | | | | |
| 446 | GAG CGC CTG GTG TCA ATC AGA AAC CGG CAG GGG ATC CAC CCG GCG AGC | 1152 | | |
| 447 | | | | |
| 448 | Glu Arg Leu Val Ser Ile Arg Asn Arg Gln Gly Ile His Pro Ala Ser | | | |
| 449 | 370 375 380 | | | |
| 450 | | | | |
| 451 | GAG CTG CGC ATC ATG GAA GCT GAC AGC GAT CTC TAC CTC GCG GAG ATC | 1200 | | |
| 452 | | | | |
| 453 | Glu Leu Arg Ile Met Glu Ala Asp Ser Asp Leu Tyr Leu Ala Glu Ile | | | |
| 454 | 385 390 395 | | | |
| 455 | | | | |
| 456 | GAT GGC AAG GTG ATC ACA AAG ATT GGA CCA AGA TAC GAC GTC GAA CAC | 1248 | | |
| 457 | | | | |
| 458 | Asp Gly Lys Val Ile Thr Lys Ile Gly Pro Arg Tyr Asp Val Glu His | | | |
| 459 | 400 405 410 | | | |

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DATE: 10/28/93
TIME: 14:01:32

INPUT SET: S6832.raw

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460
461 CTC ATC CCC GAA GGC TTC CAG GTC GTC GCG CAC GGT GAT GGC TAC GCA      1296
462
463 Leu Ile Pro Glu Gly Phe Gln Val Val Ala His Gly Asp Gly Tyr Ala
464     415                      420                      425
465
466 ATC TGG GAG AAA ATC TGAGCGCACG ATGACGAGAC TCTCAGTTTA GCAGATTTAA      1351
467
468 Ile Trp Glu Lys LIe
469 430                      435
470
471 CCTGCGATTT TTACCCTGAC CGGTATACGT ATATACGTGC CGGCAACGAG CTGTATCCGA      1411
472
473
474 TCCGAATTAC GGATGCAATT GTCCACGAAG TCCTCGAGG      1450
475
476
477
478 (2) INFORMATION FOR SEQ ID NO: 6:
479
480 (i) SEQUENCE CHARACTERISTICS:
481 (A) LENGTH: 434 amino acids
482 (B) TYPE: amino acid
483 (D) Topology: linear
484
485 (ii) MOLECULE TYPE: protein
486
487 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
488
489 Met Gln Val Leu Asn Thr Met Val Asn Lys His Phe Leu Ser Leu Ser
490   1             5             10             15
491
492 Val Leu Ile Val Leu Leu Gly Leu Ser Ser Asn Leu Thr Ala Gly Gln
493           20             25             30
494
495 Val Leu Phe Gln Gly Phe Asn Trp Glu Ser Trp Lys Glu Asn Gly Gly
496       35             40             45
497
498 Trp Tyr Asn Phe Leu Met Gly Lys Val Asp Asp Ile Ala Ala Ala Gly
499       50             55             60
500
501 Ile Thr His Val Trp Leu Pro Pro Pro Ser His Ser Val Gly Glu Gln
502       65             70             75             80
503
504 Gly Tyr Met Pro Gly Arg Leu Tyr Asp Leu Asp Ala Ser Lys Tyr Gly
505           85             90             95
506
507 Asn Glu Ala Gln Leu Lys Ser Leu Ile Glu Ala Phe His Gly Lys Gly
508       100            105            110
509
510 Val Gln Val Ile Ala Asp Ile Val Ile Asn His Arg Thr Ala Glu His

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RAW SEQUENCE LISTING PATENT APPLICATION US/07/923,692C

DATE: 10/28/93
TIME: 14:01:39

INPUT SET: S6832.raw

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511          115          120          125
512
513 Lys Asp Gly Arg Gly Ile Tyr Cys Leu Phe Glu Gly Gly Thr Pro Asp
514      130          135          140
515
516 Ser Arg Leu Asp Trp Gly Pro His Met Ile Cys Arg Asp Asp Pro Tyr
517 145          150          155          160
518
519 Gly Asp Gly Thr Gly Asn Pro Asp Thr Gly Ala Asp Phe Ala Ala Ala
520          165          170          175
521
522 Pro Asp Ile Asp His Leu Asn Lys Arg Val Gln Arg Glu Leu Ile Gly
523      180          185          190
524
525 Trp Leu Asp Trp Leu Lys Met Asp Ile Gly Phe Asp Ala Trp Arg Leu
526      195          200          205
527
528 Asp Phe Ala Lys Gly Tyr Ser Ala Asp Met Ala Lys Ile Tyr Ile Asp
529 210          215          220
530
531 Ala Thr Glu Pro Ser Phe Ala Val Ala Glu Ile Trp Thr Ser Met Ala
532 225          230          235          240
533
534 Asn Gly Gly Asp Gly Lys Pro Asn Tyr Asp Gln Asn Ala His Arg Gln
535      245          250          255
536
537 Glu Leu Val Asn Trp Val Asp Arg Val Gly Gly Ala Asn Ser Asn Gly
538      260          265          270
539
540 Thr Ala Phe Asp Phe Thr Thr Lys Gly Ile Leu Asn Val Ala Val Glu
541      275          280          285
542
543 Gly Glu Leu Trp Arg Leu Arg Gly Glu Asp Gly Lys Ala Pro Gly Met
544 290          295          300
545
546 Ile Gly Trp Trp Pro Ala Lys Ala Thr Thr Phe Val Asp Asn His Asp
547 305          310          315          320
548
549 Thr Gly Ser Thr Gln His Leu Trp Pro Phe Pro Ser Asp Lys Val Met
550      325          330          335
551
552 Gln Gly Tyr Ala Tyr Ile Leu Thr His Pro Gly Asn Pro Cys Ile Phe
553      340          345          350
554
555 Tyr Asp His Phe Phe Asp Trp Gly Leu Lys Glu Glu Ile Glu Arg Leu
556      355          360          365
557
558 Val Ser Ile Arg Asn Arg Gln Gly Ile His Pro Ala Ser Glu Leu Arg
559      370          375          380
560
561 Ile Met Glu Ala Asp Ser Asp Leu Tyr Leu Ala Glu Ile Asp Gly Lys

```

RAW SEQUENCE LISTING
PATENT APPLICATION US/07/923,692CDATE: 10/28/93
TIME: 14:01:46

INPUT SET: S6832.raw

562 385 390 395 400
563
564 Val Ile Thr Lys Ile Gly Pro Arg Tyr Asp Val Glu His Leu Ile Pro
565 405 410 415
566
567 Glu Gly Phe Gln Val Val Ala His Gly Asp Gly Tyr Ala Ile Trp Glu
568 420 425 430
569
570 Lys Ile
571
572

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 709 base pairs
(B) TYPE: nucleic acid
(G) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens
- (vii) IMMEDIATE SOURCE:
(B) CLONE: alpha-hemoglobin
- (ix) FEATURE:
(A) NAME/KEY: transit_peptide (B)
LOCATION: 26. .241
(B) LOCATION: 26. .241
- (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 245. .670

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

604 CTCGAGGGCA TCTGATCTTT CAAGAATGGC ACAAATTAAC AACATGGCAC AAGGGATACA 60
605
606 AACCCCTTAAT CCCAATTCCA ATTTCCATAA ACCCCAAGTT CCTAAATCTT CAAGTTTCTT 120
607
--> 608 TGT TTTTGGGA TGTA AAAAAC TGAAAAATTC AGCAAATTCT ATGTTGGTTT TGAAAAAAGA 180
609
--> 610 TTCAATTTT ATGCAAAAGT TTTGTTCTT TAGGATTTC A GCAGGTGGTA GAGTTTCTTG 240
611
612 CATG GTG CTG TCT CCT GCC GAC AAG ACC AAC GTC AAG GCC GCC TGG GGC 289

Change this letter "o"
into the number "0" (zero).

RAW SEQUENCE LISTING
PATENT APPLICATION US/07/923,692CDATE: 10/28/93
TIME: 14:01:53

INPUT SET: S6832.raw

613
614 Val Leu Ser Pro Ala Asp Lys Thr Asn Val Lys Ala Ala Trp Cly
615 1 5 10 15
616
617 AAG GTT GGC GCG CAC GCT GGC GAG TAT GGT GCG GAG GCC CTG GAG AGG 337
618
619 Lys Val Gly Ala His Ala Gly Glu Tyr Gly Ala Glu Ala Leu Glu Arg
620 20 25 30
621
622 ATG TTC CTG TCC TTC CCC ACC ACC AAG ACC TAC TTC CCG CAC TTC GAC 385
623
624 Met Phe Leu Ser Phe Pro Thr Thr Lys Thr Tyr Phe Pro His Phe Asp
625 35 40 45
626
627 CTG AGC CAC GGC TCT GCC CAG GTT AAG GGC CAC GGC AAG AAG GTG GCC 433
628
629 Leu Ser His Gly Ser Ala Gln Val Lys Gly His Gly Lys Lys Val Ala
630 50 55 60
631
632 GAC GCG CTG ACC AAC GCC GTG GCG CAC GTG GAC GAC ATG CCC AAC GCG 481
633
634 Asp Ala Leu Thr Asn Ala Val Ala His Val Asp Asp Met Pro Asn Ala
635 65 70 75
636
637 CTG TCC GCC CTG AGC GAC CTG CAC GCG CAC AAG CTT CGG GTG GAC CCG 529
638
639 Leu Ser Ala Leu Ser Asp Leu His Ala His Lys Leu Arg Val Asp Pro
640 80 85 90 95
641
642 GTC AAC TTC AAG CTC CTA AGC CAC TGC CTG CTG GTG ACC CTG GCC GCC 577
643
644 Val Asn Phe Lys Leu Leu Ser His Cys Leu Leu Val Thr Leu Ala Ala
645 100 105 110
646
647 CAC CTC CCC GCC GAG TTC ACC CCT GCG GTG CAC GCC TCC CTG GAC AAG 625
648
649 His Leu Pro Ala Glu Phe Thr Pro Ala Val His Ala Ser Leu Asp Lys
650 115 120 125
651
652 TTC CTG GCT TCT GTG AGC ACC GTG CTG ACC TCC AAA TAC CGT TAAGCTGGAG 677
653
654 Phe Leu Ala Ser Val Ser Thr Val Leu Thr Ser Lys Tyr Arg
655 130 135 140
656
657
658 CCTCGGTAGC CGTTCCTCCT GCCCGGTCTGA CC 709
659
660
661 (2) INFORMATION FOR SEQ ID NO:8:
662
663 (i) SEQUENCE CHARACTERISTICS:

RAW SEQUENCE LISTING
PATENT APPLICATION US/07/923,692CDATE: 10/28/93
TIME: 14:02:00

INPUT SET: S6832.raw

664 (A) LENGTH: 141 amino acids
665 (B) TYPE: amino acid
666 (D) TOPOLOGY: linear
667
668 (ii) MOLECULE TYPE: protein
669
670
671 (ix) SEQUENCE DESCRIPTION: SEQ ID NO:8:
672
673 Val Leu Ser Pro Ala Asp Lys Thr Asn Val Lys Ala Ala Trp Gly Lys
674 1 5 10 15
675
676 Val Gly Ala His Ala Gly Glu Tyr Gly Ala Glu Ala Leu Glu Arg Met
677 20 25 30
678
679 Phe Leu Ser Phe Pro Thr Thr Lys Thr Tyr Phe Pro His Phe Asp Leu
680 35 40 45
681
682 Ser His Gly Ser Ala Gln Val Lys Gly His Gly Lys Lys Val Ala Asp
683 50 55 60
684
685 Ala Leu Thr Asn Ala Val Ala His Val Asp Asp Met Pro Asn Ala Leu
686 65 70 75 80
687
688 Ser Ala Leu Ser Asp Leu His Ala His Lys Leu Arg Val Asp Pro Val
689 85 90 95
690
691 Asn Phe Lys Leu Leu Ser His Cys Leu Leu Val Thr Leu Ala Ala His
692 100 105 110
693
694 Leu Pro Ala Glu Phe Thr Pro Ala Val His Ala Ser Leu Asp Lys Phe
695 115 120 125
696
697 Leu Ala Ser Val Ser Thr Val Leu Thr Ser Lys Tyr Arg
698 130 135 140
699
700

(2) INFORMATION FOR SEQ ID NO:9:

701
702
703 (i) SEQUENCE CHARACTERISTICS:
704 (A) LENGTH: 743 base pairs
705 (B) TYPE: nucleic acid
706 (C) STRANDEDNESS: single
707 (D) TOPOLOGY: linear
708
709 (ii) MOLECULE TYPE: cDNA to mRNA
710
711 (iii) HYPOTHETICAL: NO
712
713 (iv) ANTI-SENSE: NO
714

RAW SEQUENCE LISTING PATENT APPLICATION US/07/923,692C

DATE: 10/28/93
TIME: 14:02:07

INPUT SET: S6832.raw

```

715 (vi) ORIGINAL SOURCE:
716 (A) ORGANISM: Homo sapiens
717
718 (vii) IMMEDIATE SOURCE:
719 (B) CLONE: beta-hemoglobin
720
721 (ix) FEATURE:
722 (A) NAME/KEY: transit_peptide (B)
723 LOCATION: 26..241
724 (B) LOCATION: 26..241
725
726 (ix) FEATURE:
727 (A) NAME/KEY: CDS
728 (B) LOCATION: 245..685
729
730 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
731
732 CTCGAGGGGA TCTGATCTTT CAAGAATGGC ACAAATTAAC AACATGGCAC AAGGGATACA 60
733
734 AACCCCTTAAT CCCAATTCCA ATTTCCATAA ACCCCAAGTT CCTAAATCTT CAAGTTTTCT 120
735
736 TGTTTTTTGGA TCTAAAAAAC TGAAAAATTC AGCAAATTCT ATGTTGGTTT TGAAAAAAGA 180
737
738 TTCAATTTTT ATGCAAAAGT TTTGTTCTT TAGGATTTCA GCAGGTGGTA GAGTTTCTTG 240
739
740 GATG GTG CAC CTG ACT CCT GAG GAG AAG TCT GCC GTT ACT GCC CTG TGG 289
741
742 Val His Leu Thr Pro Glu Glu Lys Ser Ala Val Thr Ala Leu Trp
743 1 5 10 15
744
745 GGC AAG GTG AAC GTG GAT GAA GTT GGT GGT GAG GCC CTG GGC AGG CTG 337
746
747 Gly Lys Val Asn Val Asp Glu Val Gly Gly Glu Ala Leu Gly Arg Leu
748 20 25 30
749
750 CTG GTG GTC TAC CCT TGG ACC CAG AGG TTC TTT GAG TCC TTT GGG GAT 385
751
752 Leu Val Val Tyr Pro Trp Thr Gln Arg Phe Phe Glu Ser Phe Gly Asp
753 35 40 45
754
755 CTG TCC ACT CCT GAT GCT GTT ATG GGC AAC CCT AAG GTG AAG GCT CAT 433
756
757 Leu Ser Thr Pro Asp Ala Val Met Gly Asn Pro Lys Val Lys Ala His
758 50 55 60
759
760 GGC AAG AAA GTG CTG GGT GCC TTT AGT GAT GGC CTG GCT CAC CTG GAC 481
761
762 Gly Lys Lys Val Leu Gly Ala Phe Ser Asp Gly Leu Ala His Leu Asp
763 65 70 75
764
765 AAC CTC AAG GGC ACC TTT GCC ACC CTG AGT GAG CTG CAC TGT GAC AAG 529

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RAW SEQUENCE LISTING PATENT APPLICATION US/07/923,692C

DATE: 10/28/93
TIME: 14:02:13

INPUT SET: S6832.raw

```

766
767 Asn Leu Lys Gly Thr Phe Ala Thr Leu Ser Glu Leu His Cys Asp Lys
768 80 85 90 95
769
770 CTG CAC GTG GAT CCT GAG AGC TTC AGG CTC CTA GGC AAC GTG CTG GTC 577
771
772 Leu His Val Asp Pro Glu Ser Phe Arg Leu Leu Gly Asn Val Leu Val
773 100 105 110
774
775 TGT GTG CTG GCG CAT CAC TTT GGC AAA GAA TTC ACC CCA CCA GTG CAG 625
776
777 Cys Val Leu Ala His His Phe Gly Lys Glu Phe Thr Pro Pro Val Gln
778 115 120 125
779
780 GCT GCC TAT CAG AAA GTG GTG GCT GGT GTG GCT AAT GCC CTG GCC CAC 673
781
782 Ala Ala Tyr Gln Lys Val Val Ala Gly Val Ala Asn Ala Leu Ala His
783 130 135 140
784
785 AAG TAT CAC TAAGCTCGCT TTCTTGCTGT CCAATTTCTA TTAAAGGTTC 722
786
787 Lys Tyr His
788 145
789
790 CTTTGTGGGG TCGAGGTCTGA C 743
791
792
793
794 (2) INFORMATION FOR SEQ ID NO: 10:
795
796 (i) SEQUENCE CHARACTERISTICS:
797 (A) LENGTH: 146 amino acids
798 (B) TYPE: amino acid
799 (D) TOPOLOGY: linear
800 (ii) MOLECULE TYPE: protein
801
802 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:
803
804 Val His Leu Thr Pro Glu Glu Lys Ser Ala Val Thr Ala Leu Trp Gly
805 1 5 10 15
806
807 Lys Val Asn Val Asp Glu Val Gly Gly Glu Ala Leu Gly Arg Leu Leu
808 20 25 30
809
810 Val Val Tyr Pro Trp Thr Gln Arg Phe Phe Glu Ser Phe Gly Asp Leu
811 35 40 45
812
813 Ser Thr Pro Asp Ala Val Met Gly Asn Pro Lys Val Lys Ala His Gly
814 50 55 60
815
816 Lys Lys Val Leu Gly Ala Phe Ser Asp Gly Leu Ala His Leu Asp Asn

```


RAW SEQUENCE LISTING PATENT APPLICATION US/07/923,692C

DATE: 10/28/93
TIME: 14:02:20

INPUT SET: S6832.raw

```

817      65              70              75              80
818
819  Leu Lys Gly Thr Phe Ala Thr Leu Ser Glu Leu His Cys Asp Lys Leu
820              85              90              95
821
822  His Val Asp Pro Glu Ser Phe Arg Leu Leu Gly Asn Val Leu Val Cys
823              100              105              110
824
825  Val Leu Ala His His Phe Gly Lys Glu Phe Thr Pro Pro Val Gln Ala
826              115              120              125
827
828  Ala Tyr Gln Lys Val Val Ala Gly Val Ala Asn Ala Leu Ala His Lys
829      130              135              140
830
831  Tyr His
832      145
833
834
835  (2)  INFORMATION FOR SEQ ID NO:11:
836
837      (i)      SEQUENCE CHARACTERISTICS:
838                (A)  LENGTH: 17 amino acids
839                (B)  TYPE: amino acid
840                (D)  TOPOLOGY: linear
841
842      (ii)     MOLECULE TYPE: peptide
843
844      (v)      FRAGMENT TYPE: N-terminal
845
846      (vi)     ORIGINAL SOURCE:
847                (A)  ORGANISM: alkalophilic Bacillus sp.
848                (B)  STRAIN: 38-2
849
850      (vii)    IMMEDIATE SOURCE:
851                (B)  CLONE: beta-cyclodextrin
852
853      (xi)     SEQUENCE DESCRIPTION: SEQ ID NO: 11:
854
855  Ala Pro Asp Thr Ser Val Ser Asn Lys Gln Asn Phe Ser Thr Asp Val
856      1              5              10              15
857
858  Ile
859

```

PAGE: 1

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION US/07/923,692C

DATE: 10/28/93
TIME: 14:02:27

INPUT SET: S6832.raw

| Line | Error | Original Text |
|------|--|---|
| 31 | Wrong application Serial Number | (A) APPLICATION NUMBER: <u>US 923,692</u> |
| 608 | # of Sequences for line conflicts w/ running total | TGTTTTTGGA TGTAACAAAC TGAAATTC AGCAA |
| 610 | # of Sequences for line conflicts w/ running total | TTCAATTTT ATGCAAAAGT TTTGTTCTT TAGGAT |

PAGE: 1

SEQUENCE MISSING ITEM REPORT
PATENT APPLICATION US/07/923,692C

DATE: 10/28/93
TIME: 14:02:27

INPUT SET: S6832.raw

COUNTRY
PRIOR APPLICATION DATA More Identifiers Found Than MAX Allowed

PAGE: 1

SEQUENCE CORRECTION REPORT
PATENT APPLICATION US/07/923,692C

DATE: 10/28/93
TIME: 14:02:27

INPUT SET: S6832.raw

| Line | Original Text | Corrected Text |
|------|---------------|----------------|
|------|---------------|----------------|